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RAW SEQUENCE LISTING

DATE: 02/11/2002

PATENT APPLICATION: US/10/044,716

TIME: 10:05:07

Input Set : A:\270-070US.ST25.txt

Output Set: N:\CRF3\02112002\J044716.raw

3 <110> APPLICANT: LANGENFELD, John
 5 <120> TITLE OF INVENTION: BONE MORPHOGENETIC PROTEIN-2 IN THE TREATMENT AND DIAGNOSIS
 OF CANCER

7 <130> FILE REFERENCE: 270/070US
 C--> 9 <140> CURRENT APPLICATION NUMBER: US/10/044,716
 10 <141> CURRENT FILING DATE: 2002-01-11
 12 <150> PRIOR APPLICATION NUMBER: US60/261,252
 13 <151> PRIOR FILING DATE: 2001-01-12
 15 <160> NUMBER OF SEQ ID NOS: 16
 17 <170> SOFTWARE: PatentIn version 3.1
 19 <210> SEQ ID NO: 1
 20 <211> LENGTH: 1547
 21 <212> TYPE: DNA
 22 <213> ORGANISM: Homo sapiens
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 25 <221> NAME/KEY: source
 26 <222> LOCATION: (1)..(1547)
 27 <223> OTHER INFORMATION: Homo sapiens: Taxon:9606
 30 <220> FEATURE:
 31 <221> NAME/KEY: gene
 32 <222> LOCATION: (1)..(1547)
 33 <223> OTHER INFORMATION: BMP2
 36 <220> FEATURE:
 37 <221> NAME/KEY: CDS
 38 <222> LOCATION: (324)..(1514)
 39 <223> OTHER INFORMATION:
 42 <220> FEATURE:
 43 <221> NAME/KEY: misc_feature
 44 <222> LOCATION: (429)..(1127)
 45 <223> OTHER INFORMATION: Region: TGF-beta propeptide
 48 <220> FEATURE:
 49 <221> NAME/KEY: variation
 50 <222> LOCATION: (432)..(432)
 51 <223> OTHER INFORMATION: Allele = "T"; Allele = "G"
 54 <220> FEATURE:
 55 <221> NAME/KEY: variation
 56 <222> LOCATION: (584)..(584)
 57 <223> OTHER INFORMATION: Allele = "A"; Allele = "G"
 60 <220> FEATURE:
 61 <221> NAME/KEY: variation
 62 <222> LOCATION: (893)..(893)
 63 <223> OTHER INFORMATION: Allele = "T"; Allele = "A"
 66 <220> FEATURE:
 67 <221> NAME/KEY: misc_feature

ENTERED

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68 <222> LOCATION: (1209)..(1511)

69 <223> OTHER INFORMATION: TGF-beta; Region: Transforming growth factor beta like domain

72 <220> FEATURE:

73 <221> NAME/KEY: misc_feature

74 <222> LOCATION: (1209)..(1511)

75 <223> OTHER INFORMATION: TGFB; Region: Transforming growth factor-beta (TGF-beta)

family

78 <400> SEQUENCE: 1

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81 tgccccagcg gagctgctt cgccatctcc gagccccacc gccctccac tcctcggcct      120
83 tgcccgacac tgagacgctg ttccagcgt gaaaagagag actgcgcggc cggcaccgcg      180
85 gagaaggagg aggcaaagaa aaggaaacgga cattcggtcc ttgcgccagg tcctttgacc      240
87 agagtttttc catgtggacg ctctttcaat ggacgtgtcc ccgcgtgctt cttagacgga      300
89 ctgcggtctc cttaaaggctg acc atg gtg gcc ggg acc cgc tgt ctt cta gcg      353
90                               Met Val Ala Gly Thr Arg Cys Leu Leu Ala
91                               1                               5                               10
93 ttg ctg ctt ccc cag gtc ctc ctg ggc ggc gcg gct ggc ctc gtt ccg      401
94 Leu Leu Leu Pro Gln Val Leu Leu Gly Gly Ala Ala Gly Leu Val Pro
95                               15                               20                               25
97 gag ctg ggc cgc agg aag ttc gcg gcg gcg tcg tcg ggc cgc ccc tca      449
98 Glu Leu Gly Arg Arg Lys Phe Ala Ala Ala Ser Ser Gly Arg Pro Ser
99                               30                               35                               40
101 tcc cag ccc tct gac gag gtc ctg agc gag ttc gag ttg cgg ctg ctc      497
102 Ser Gln Pro Ser Asp Glu Val Leu Ser Glu Phe Glu Leu Arg Leu Leu
103                               45                               50                               55
105 agc atg ttc ggc ctg aaa cag aga ccc acc ccc agc agg gac gcc gtg      545
106 Ser Met Phe Gly Leu Lys Gln Arg Pro Thr Pro Ser Arg Asp Ala Val
107                               60                               65                               70
109 gtg ccc ccc tac atg cta gac ctg tat cgc agg cac tca ggt cag ccg      593
110 Val Pro Pro Tyr Met Leu Asp Leu Tyr Arg Arg His Ser Gly Gln Pro
111 75                               80                               85                               90
113 ggc tca ccc gcc cca gac cac cgg ttg gag agg gca gcc agc cga gcc      641
114 Gly Ser Pro Ala Pro Asp His Arg Leu Glu Arg Ala Ala Ser Arg Ala
115                               95                               100                              105
117 aac act gtg cgc agc ttc cac cat gaa gaa tct ttg gaa gaa cta cca      689
118 Asn Thr Val Arg Ser Phe His His Glu Glu Ser Leu Glu Glu Leu Pro
119                               110                              115                              120
121 gaa acg agt ggg aaa aca acc cgg aga ttc ttc ttt aat tta agt tct      737
122 Glu Thr Ser Gly Lys Thr Thr Arg Arg Phe Phe Phe Asn Leu Ser Ser
123                               125                              130                              135
125 atc ccc acg gag gag ttt atc acc tca gca gag ctt cag gtt ttc cga      785
126 Ile Pro Thr Glu Glu Phe Ile Thr Ser Ala Glu Leu Gln Val Phe Arg
127                               140                              145                              150
129 gaa cag atg caa gat gct tta gga aac aat agc agt ttc cat cac cga      833
130 Glu Gln Met Gln Asp Ala Leu Gly Asn Asn Ser Ser Phe His His Arg
131 155                              160                              165                              170
133 att aat att tat gaa atc ata aaa cct gca aca gcc aac tcg aaa ttc      881
134 Ile Asn Ile Tyr Glu Ile Ile Lys Pro Ala Thr Ala Asn Ser Lys Phe
135                               175                              180                              185
137 ccc gtg acc aga ctt ttg gac acc agg ttg gtg aat cag aat gca agc      929

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138 Pro Val Thr Arg Leu Leu Asp Thr Arg Leu Val Asn Gln Asn Ala Ser
139          190          195          200
141 agg tgg gaa agt ttt gat gtc acc ccc gct gtg atg cgg tgg act gca      977
142 Arg Trp Glu Ser Phe Asp Val Thr Pro Ala Val Met Arg Trp Thr Ala
143          205          210          215
145 cag gga cac gcc aac cat gga ttc gtg gtg gaa gtg gcc cac ttg gag      1025
146 Gln Gly His Ala Asn His Gly Phe Val Val Glu Val Ala His Leu Glu
147          220          225          230
149 gag aaa caa ggt gtc tcc aag aga cat gtt agg ata agc agg tct ttg      1073
150 Glu Lys Gln Gly Val Ser Lys Arg His Val Arg Ile Ser Arg Ser Leu
151 235          240          245          250
153 cac caa gat gaa cac agc tgg tca cag ata agg cca ttg cta gta act      1121
154 His Gln Asp Glu His Ser Trp Ser Gln Ile Arg Pro Leu Leu Val Thr
155          255          260          265
157 ttt ggc cat gat gga aaa ggg cat cct ctc cac aaa aga gaa aaa cgt      1169
158 Phe Gly His Asp Gly Lys Gly His Pro Leu His Lys Arg Glu Lys Arg
159          270          275          280
161 caa gcc aaa cac aaa cag cgg aaa cgc ctt aag tcc agc tgt aag aga      1217
162 Gln Ala Lys His Lys Gln Arg Lys Arg Leu Lys Ser Ser Cys Lys Arg
163          285          290          295
165 cac cct ttg tac gtg gac ttc agt gac gtg ggg tgg aat gac tgg att      1265
166 His Pro Leu Tyr Val Asp Phe Ser Asp Val Gly Trp Asn Asp Trp Ile
167          300          305          310
169 gtg gct ccc ccg ggg tat cac gcc ttt tac tgc cac gga gaa tgc cct      1313
170 Val Ala Pro Pro Gly Tyr His Ala Phe Tyr Cys His Gly Glu Cys Pro
171 315          320          325          330
173 ttt cct ctg gct gat cat ctg aac tcc act aat cat gcc att gtt cag      1361
174 Phe Pro Leu Ala Asp His Leu Asn Ser Thr Asn His Ala Ile Val Gln
175          335          340          345
177 acg ttg gtc aac tct gtt aac tct aag att cct aag gca tgc tgt gtc      1409
178 Thr Leu Val Asn Ser Val Asn Ser Lys Ile Pro Lys Ala Cys Cys Val
179          350          355          360
181 ccg aca gaa ctc agt gct atc tcg atg ctg tac ctt gac gag aat gaa      1457
182 Pro Thr Glu Leu Ser Ala Ile Ser Met Leu Tyr Leu Asp Glu Asn Glu
183          365          370          375
185 aag gtt gta tta aag aac tat cag gac atg gtt gtg gag ggt tgt ggg      1505
186 Lys Val Val Leu Lys Asn Tyr Gln Asp Met Val Val Glu Gly Cys Gly
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190 Cys Arg
191 395
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195 <211> LENGTH: 396
196 <212> TYPE: PRT
197 <213> ORGANISM: Homo sapiens
199 <220> FEATURE:
200 <221> NAME/KEY: misc_feature
201 <222> LOCATION: (429)..(1127)
202 <223> OTHER INFORMATION: Region: TGF-beta propeptide

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204 <220> FEATURE:
205 <221> NAME/KEY: misc_feature
206 <222> LOCATION: (1209)..(1511)
207 <223> OTHER INFORMATION: TGF-beta; Region: Transforming growth factor beta like
domain
209 <220> FEATURE:
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211 <222> LOCATION: (1209)..(1511)
212 <223> OTHER INFORMATION: TGF-beta; Region: Transforming growth factor-beta (TGF-beta)
family
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217 1 5 10 15
220 Leu Leu Gly Gly Ala Ala Gly Leu Val Pro Glu Leu Gly Arg Arg Lys
221 20 25 30
224 Phe Ala Ala Ala Ser Ser Gly Arg Pro Ser Ser Gln Pro Ser Asp Glu
225 35 40 45
228 Val Leu Ser Glu Phe Glu Leu Arg Leu Leu Ser Met Phe Gly Leu Lys
229 50 55 60
232 Gln Arg Pro Thr Pro Ser Arg Asp Ala Val Val Pro Pro Tyr Met Leu
233 65 70 75 80
236 Asp Leu Tyr Arg Arg His Ser Gly Gln Pro Gly Ser Pro Ala Pro Asp
237 85 90 95
240 His Arg Leu Glu Arg Ala Ala Ser Arg Ala Asn Thr Val Arg Ser Phe
241 100 105 110
244 His His Glu Glu Ser Leu Glu Glu Leu Pro Glu Thr Ser Gly Lys Thr
245 115 120 125
248 Thr Arg Arg Phe Phe Phe Asn Leu Ser Ser Ile Pro Thr Glu Glu Phe
249 130 135 140
252 Ile Thr Ser Ala Glu Leu Gln Val Phe Arg Glu Gln Met Gln Asp Ala
253 145 150 155 160
256 Leu Gly Asn Asn Ser Ser Phe His His Arg Ile Asn Ile Tyr Glu Ile
257 165 170 175
260 Ile Lys Pro Ala Thr Ala Asn Ser Lys Phe Pro Val Thr Arg Leu Leu
261 180 185 190
264 Asp Thr Arg Leu Val Asn Gln Asn Ala Ser Arg Trp Glu Ser Phe Asp
265 195 200 205
268 Val Thr Pro Ala Val Met Arg Trp Thr Ala Gln Gly His Ala Asn His
269 210 215 220
272 Gly Phe Val Val Glu Val Ala His Leu Glu Glu Lys Gln Gly Val Ser
273 225 230 235 240
276 Lys Arg His Val Arg Ile Ser Arg Ser Leu His Gln Asp Glu His Ser
277 245 250 255
280 Trp Ser Gln Ile Arg Pro Leu Leu Val Thr Phe Gly His Asp Gly Lys
281 260 265 270
284 Gly His Pro Leu His Lys Arg Glu Lys Arg Gln Ala Lys His Lys Gln
285 275 280 285
288 Arg Lys Arg Leu Lys Ser Ser Cys Lys Arg His Pro Leu Tyr Val Asp
289 290 295 300
292 Phe Ser Asp Val Gly Trp Asn Asp Trp Ile Val Ala Pro Pro Gly Tyr
293 305 310 315 320

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296 His Ala Phe Tyr Cys His Gly Glu Cys Pro Phe Pro Leu Ala Asp His
297           325           330           335
300 Leu Asn Ser Thr Asn His Ala Ile Val Gln Thr Leu Val Asn Ser Val
301           340           345           350
304 Asn Ser Lys Ile Pro Lys Ala Cys Cys Val Pro Thr Glu Leu Ser Ala
305           355           360           365
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313 385           390           395
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317 <211> LENGTH: 699
318 <212> TYPE: DNA
319 <213> ORGANISM: Homo sapiens
321 <220> FEATURE:
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324 <223> OTHER INFORMATION: Homo sapiens: Taxon:9606
327 <220> FEATURE:
328 <221> NAME/KEY: gene
329 <222> LOCATION: (1)..(699)
330 <223> OTHER INFORMATION: NOG
333 <220> FEATURE:
334 <221> NAME/KEY: sig_peptide
335 <222> LOCATION: (1)..(57)
336 <223> OTHER INFORMATION:
339 <220> FEATURE:
340 <221> NAME/KEY: CDS
341 <222> LOCATION: (1)..(699)
342 <223> OTHER INFORMATION: Noggin, mouse, homolog of
345 <300> PUBLICATION INFORMATION:
346 <301> AUTHORS: Valenzuela,D.M., Economides,A.N., Rojas,E., Lamb,T.M., Nunez,L.,
Jones,P., Ip,N.Y., Espinosa,R., Brannan,C.I., Gilbert,D.J., Copeland,N.G., Jenkins,N.A.,
LeBeau,M.M., Harland,R.M. and Yancopoul
347 <302> TITLE: Identification of mammalian noggin and its expression in the adult
nervous system
348 <303> JOURNAL: J. Neurosci.
349 <304> VOLUME: 15
350 <305> ISSUE: 9
351 <306> PAGES: 6077-6084
352 <307> DATE: 1995
353 <308> DATABASE ACCESSION NO: NM_005450
354 <309> DATABASE ENTRY DATE: 2000-11-01
355 <313> RELEVANT RESIDUES: (1)..(699)
357 <300> PUBLICATION INFORMATION:
358 <301> AUTHORS: McMahon,J.A., Takada,S., Zimmerman,L.B., Fan,C.M., Harland,R.M. and
McMahon, A.P.
359 <302> TITLE: Noggin-mediated antagonism of BMP signaling is required for growth and
patterning of the neural tube and somite
360 <303> JOURNAL: Genes Dev.
361 <304> VOLUME: 12
362 <305> ISSUE: 10
363 <306> PAGES: 1438-1452

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364 <307> DATE: 1998

VERIFICATION SUMMARY

PATENT APPLICATION: US/10/044,716

DATE: 02/11/2002

TIME: 10:05:08

Input Set : A:\270-070US.ST25.txt

Output Set: N:\CRF3\02112002\J044716.raw

L:9 M:270 C: Current Application Number differs, Replaced Current Application Number